Fig. 1

```
        10                  30                  50
GTGAAGAACGAAAAAACCTTCTTTGAAGAGCTTTACGAGGCTTTAGAGGAAACCCACGAC
M  K  N  E  K  T  F  F  E  E  L  Y  E  A  L  E  E  T  H  D
        70                  90                 110
AACACCGATGCCACTAGGGGGTCAGATAGGGGGTCAGAGGACTTCTTCTTGGCCACCGAC
N  T  D  A  T  R  G  S  D  R  G  S  E  D  F  F  L  A  T  D
       130                 150                 170
CCCCCTCCAGATGGAGGTGCCGAAAATCGCCTCGCGAAGGGCTTTACATACCAAAAAGAG
P  P  P  D  G  G  A  E  N  R  L  A  K  G  F  T  Y  Q  K  E
       190                 210                 230
GCACTTAGGATTGCTTTACCCGAGAAAGACCATGAGGCTTTCCTTTCCTCTGTTGGGGCC
A  L  R  I  A  L  P  E  K  D  H  E  A  F  L  S  S  V  G  A
       250                 270                 290
CCCCCTATACCACCAGCTGAACCCCCCGTTGGGAATGTATGTCAAGCCGTCCAGGACGGG
P  P  I  P  P  A  E  P  P  V  G  N  V  C  Q  A  V  Q  D  G
       310                 330                 350
CCTCAGAAGCTTCTGGAACTCCTCCAGGAGATTGCCCGCTCCACCATCCCCTACGGCAAC
P  Q  K  L  L  E  L  L  Q  E  I  A  R  S  T  I  P  Y  G  N
       370                 390                 410
CGGGAGCTCTGGAGGAAGGTGGGGACGGTCGTCTTCATGGTCCCCCTGGAGATGTTGGCC
R  E  L  W  R  K  V  G  T  V  V  F  M  V  P  L  E  M  L  A
       430                 450                 470
CTCAACCTGGGGGTCACCCGGCAGACCGTCCACGCCTGGAAGAAGGTCCTTGAGAAAAAG
L  N  L  G  V  T  R  Q  T  V  H  A  W  K  K  V  L  E  K  K
       490                 510                 530
GGCCTGGTGGCCACCGACGTCCTTCACCAAACCGTCAACGGGGAGCGCCGGGCCATCGGC
G  L  V  A  T  D  V  L  H  Q  T  V  N  G  E  R  R  A  I  G
       550                 570                 590
ACCCTTTGGGCCGTCCGGCTGAGGCCAGGGAAAGCCAGGCTCACCCTGGACGACTACATC
T  L  W  A  V  R  L  R  P  G  K  A  R  L  T  L  D  D  Y  I
       610                 630                 650
TACCCCTGGAGGAACCTCGCCCTAGACATGGCCAACGGCGTGCTCTCCTTCAACTGGGTC
Y  P  W  R  N  L  A  L  D  M  A  N  G  V  L  S  F  N  W  V
       670                 690                 710
AAGGCCTACCAGGACCACGGAATCCGCCCCACCCTGGACGTGCTGGTCCTCTGGGCTCAG
K  A  Y  Q  D  H  G  I  R  P  T  L  D  V  L  V  L  W  A  Q
       730                 750                 770
GGGAAAAGGGTGATGCCCAACACCAAGACCGTGGCCGTTGACCTGGGCCTCATCCTGGTC
G  K  R  V  M  P  N  T  K  T  V  A  V  D  L  G  L  I  L  V
       790                 810                 830
CTCCCCGAGGTGGAGCGTTCCAAACTCCCGGCCCTTATCACCCTCATTGCTACGTACATT
L  P  E  V  E  R  S  K  L  P  A  L  I  T  L  I  A  T  Y  I
       850                 870                 890
GCCGATCTCCTAGATGACCGTCGTTCAAGACGTTTCTATGCAGGCTTGCTGTGGGCTGTG
A  D  L  L  D  D  R  R  S  R  R  F  Y  A  G  L  L  W  A  V
       910                 930                 950
GCCAGGGGTGAACTCCCCGCGCAATATCTATTTGCCGTCCTAATGCGGGTTATCCGAGAT
A  R  G  E  L  P  A  Q  Y  L  F  A  V  L  M  R  V  I  R  D
       970                 990                1010
TACACGGATGGCCATCTGACACGACCGGGAGCGTACCTAGTGAAGACCCTCAAGGAGGCC
Y  T  D  G  H  L  T  R  P  G  A  Y  L  V  K  T  L  K  E  A

TCCTGA
S  *
```

Fig. 2

1 CTATAACGGCCTTTTAGGAGGGGGATTGCCAGCCGCTGGGCTGACGGTTATTTTGGACC

61 CATAAAAAGGCGAAACCGAGGCGGTTGCCCCGGATCACCCCCAAGACCTAGGGTAACGCC

121 TCGGGCTCCAGATGACAA*GGAGG*TCCGAGGGTGAAGAACGAAAAAACCTTCTTTGAAGAG

M K N E K T F F...(RepT)

Fig. 3

```
   1 tctagaaggt cagggtggac aaggaaaaca ccatagcccc tgccaagaag atggacgagt
  61 tggtgtccgg aaaagtggcc atccgggcg ctcttgacaa ctattttcca gcggtggcca
 121 ccggcattgg ccacgaggta cgagcttgtg gagtagacgg ccacaaaggg gtcgtcctca
 181 aacttctttt ctagtgccgc ttggacgaag gggaggaaga ggaaaggctt catggcctca
 241 cctccttccc ctcctccttg gcggccttag cggcgtaaaa ctctgagacg gcctgaagtt
 301 tagggatttc gctttcgggg ataagaatcc ggcggctcag gggatgccgg atggccctta
 361 tcctgccgtc ccttatgtac tcgtaaatgg tggccttggg tactttaaac cgttctgaaa
 421 cttctctaac agagagcaca aaacctctaa aaacctatca atcccaccga ttccagtata
 481 ccataaatgg cacaaagttt tgagaaggtg gtcaaacaaa aaggctttct cggtcaggtt
 541 atggtgaggt gggggcggtc aaaggccgac ttaagtttgg taaagccggg aggaagcaaa
 601 ccggggtgtt accatgcaac agatggccga gtggaacgtg tggacacaga gaagcgttga
 661 gcttctggag aaggggtatt tggataaact actgcaggtc tataaagggg aaagtggctc
 721 ttcgaggtca gtaccagagg aggtagagga aaaacttcgc gaggcctaca aggcatacga
 781 ggggaggcag gatagtccgg aggcagaaac gaaactcgtg gaagccgtgc taaatgccag
 841 aaaaaaggtc gagcggtccc ccttcaatca cccctacctg cctttggtct actacctggt
 901 ttcggaaaaa gcagaaaaag cgaacaaggc ccttgaggag gcattgcagg aggttgcctc
 961 aaagcaccca gaaaccatcc gcgtcctggc caaggaagcg caaagaagag gcgtagaagc
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1081 aaggtggtac aaagaagagc taaaggggaa aatagaagag aggcttccag gccctaccaa
1141 accaaagatt gtggtagtat cccctgaaaa aagtaaaccg gagcaagcac cccttattgc
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1321 cgtggtcatc cggcgtagcc ctgaagagac atggcaccta acaggagaag tgaagtttca
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1441 ggaccttgag aagaggcaca taggaatagt ggtggtggac ggaatgcctg tggtgagcaa
1501 gtttcgtggg tgggccggac tggggaaaga aacgatcgtt acatccgtac tcctccttcc
1561 agacctgata gcggagctct accaaaaggg tgaagaagcc ctgggcctct agaaggcgga
1621 cacaatctca aacttgtgct gtagcctggg gaaatcctct aacacccttc tagtgaaggc
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3241 gggagttcac ccctggccac agcccacagc aagcctgcat agaaacgtct tgaacgacgg
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```

Fig. 3 (continued)

```
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3421 ggcatcaccc ttttcccctg agcccagagg accagcacgt ccagggtggg gcggattccg
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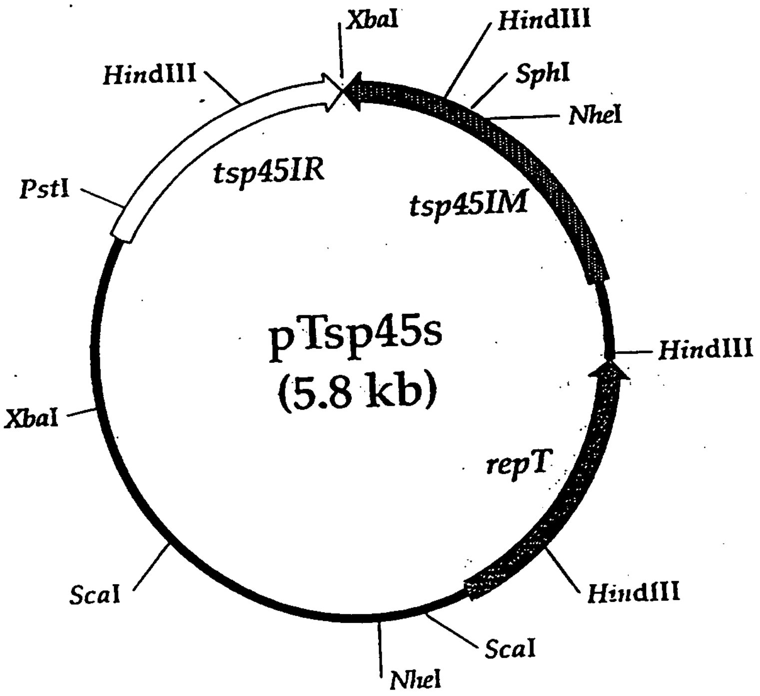
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ScaI
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Fig. 4

Fig. 5

1 ATGATCGTGGCTGTCACCGGCTTCAAGGGAGGGGTGGGGAAGACCACCACGGCGGTCCAC
M I V A V T G F K G G V G K T T T A V H
61 CTGGCCTGCTTCCTGGCCGAGCGGGGCCCCACCCTGCTGGTGGACGGGGACCCCAACCGC
L A C F L A E R G P T L L V D G D P N R
121 TCCGCCACGGGGTGGCACCGGAGGGGAGGCCTCCCGGTGACCGTGGTGGACGAGCGGGTG
S A T G W H R R G G L P V T V V D E R V
181 GCGGCCCGGTACGCCCGGGAGCACGCCCACGTGGTCATAGACACCCAGGCCCGCCCCACG
A A R Y A R E H A H V V I D T Q A R P T
241 GAAGAGGACCTCCGGGCCCTCGCCAAGGGGGTGGACCTGCTGGTCCTGCCCACGTCCCCC
E E D L R A L A K G V D L L V L P T S P
301 GACGCCCTGGCCCTGGAGGCCCTCCTGGCCACCCTGGAAGCCCTGCGGGGGGCGGAGGCC
D A L A L E A L L A T L E A L R G A E A
361 CGCTTCCGGGTCCTCCTGACCATGGTGCCCCCGCCCCCGAGCCGGGACGGGGAGGAGGCC
R F R V L L T M V P P P P S R D G E E A
421 CGGGCCCTCTTGGGGGCGGAGGGCGTTCCCCTCTTCACAGGCTGGGTGAGGCGGGCGGCA
R A L L G A E G V P L F T G W V R R A A
481 GCCTTCCCCAAGGCCGCCCTCCTGGGGGTGCCTGTCTACCGGGTGCCCGACCCCAGGGCG
A F P K A A L L G V P V Y R V P D P R A
541 AGGCTGGCCTGGGGGGACTACGCGCGGGTGGGGGAAGAGCTCCTGAAGGAGGTGGGGGA
R L A W G D Y A R V G E E L L K E V G G
601 TGA 603

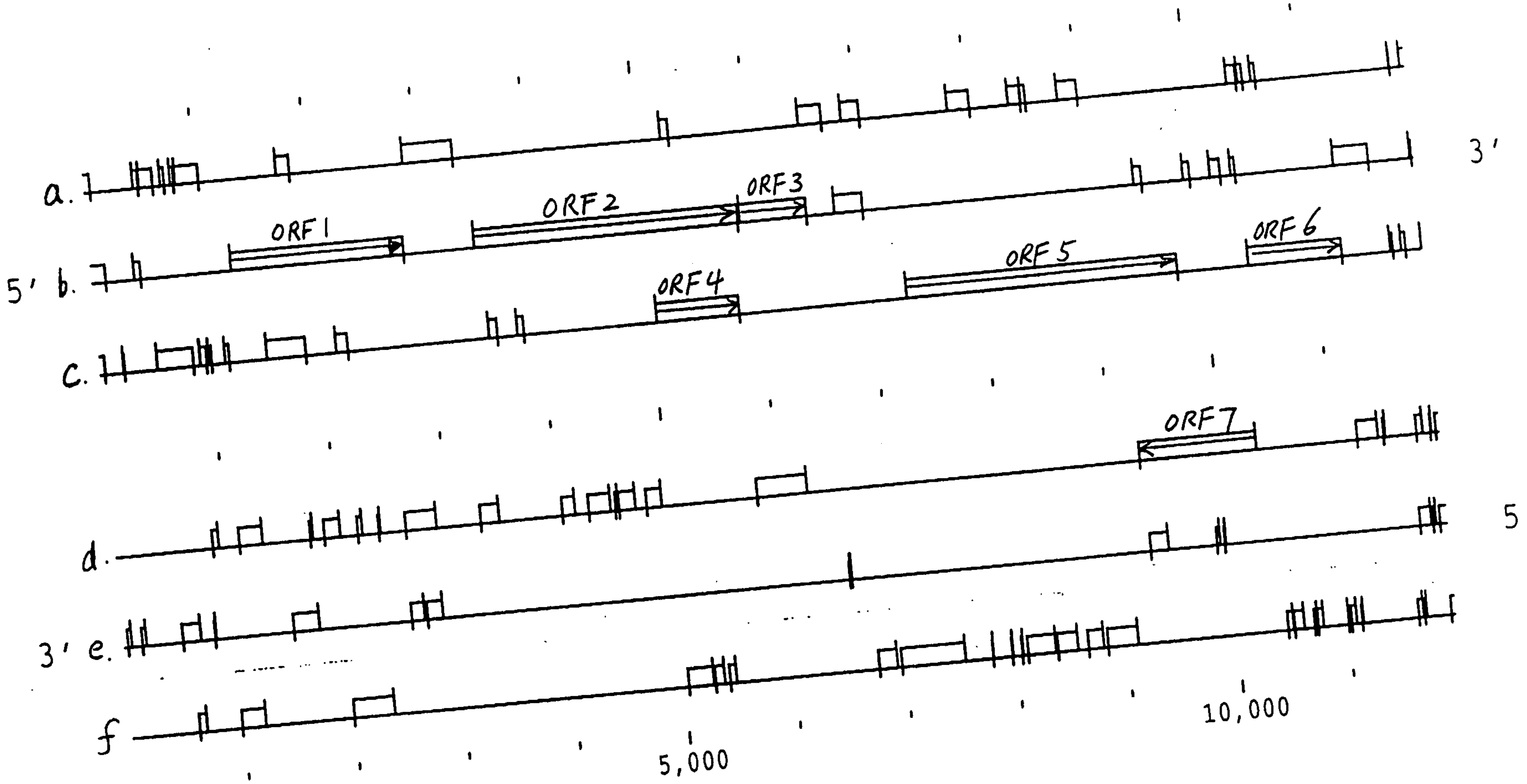

Fig. 6

Fig. 7

```
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   1   ---------+---------+---------+---------+---------+---------+   60
       CCTCCCATCTCCGGGTGTTTACAGCGGATACGGGAGGTTCAGCGGGAACTTTTCCCCTTG
  61   ---------+---------+---------+---------+---------+---------+   120
       TTGAAACTTTGGGGTCTGAGGCTCAACAGCAGAACAGCTTAGGTTGACTCAACACAGCTC
 121   ---------+---------+---------+---------+---------+---------+   180
       ATAAGTCCCTTCATTATCGCCTGAGTCAACCTATGAGTTAACCTTTTTTCAAGAAAAAGA
 181   ---------+---------+---------+---------+---------+---------+   240
       GATAAGTGAGTTTTGTCCTCTAGCACGACTTTTTTCTTTGAGTCAACCTCTGTGCCGACC
 241   ---------+---------+---------+---------+---------+---------+   300
       CCCCCGATTTTGAGTCAACCCCCCTTTGAGCCGAAACTTTGTTGGCACAGGGGTTGACTC
 301   ---------+---------+---------+---------+---------+---------+   360
       AGGGGTTGACTCAACGCGAATGGCCTCTGGAAGGGCGTTGAGCCGACCCCTCCCTCGTGT
 361   ---------+---------+---------+---------+---------+---------+   420
       GCCGACCCCCGCTCCACTATGAGCAGGGGGGAAAGTTACGGAAAAGTTCCCCAAGTCCC
 421   ---------+---------+---------+---------+---------+---------+   480
       CCTTGACAAAAGATGACAATCGAGTTAATGTCACAGCGATGCGTCACTCACCTCTGGCTG
 481   ---------+---------+---------+---------+---------+---------+   540
       GGCTCACCCAGATGCGTGCGCGAACGTTTCAGAGCCTCCTTCGATTCCTGGCCAGGGAGG
 541   ---------+---------+---------+---------+---------+---------+   600
       GGCGCTACCCCACTGGTGTAGAGCTCGCCAAGGTGCTGGGGCGCAGCCCGCACGCCACGT
 601   ---------+---------+---------+---------+---------+---------+   660
       GGGCCATGCTCAGGGCTTTGACCCGTCATGGACTCGTGGAACGGCACGAGGGGGTCTATG
 661   ---------+---------+---------+---------+---------+---------+   720
       TTCTGACCCCTGCGGGCGTAGAACTTGCCAGGACCCTGGGAACCACCGTGTGGCGTGGGG
 721   ---------+---------+---------+---------+---------+---------+   780
       ATGAGGAGGTACAGACGGCGTTACAGCTGCTAGGAGTCGGTCATGCCGCCGAGGACAGGC
 781   ---------+---------+---------+---------+---------+---------+   840
       GCTGAAGCTTTTGAGCCGGGGCCCTCACCCAAGGCCACCCCGGCTCCTCTCCCCTGGGAT
 841   ---------+---------+---------+---------+---------+---------+   900
       CCCAAATGGATCCCTCAGCGCCATTATCCTCCTGGCGGTCCTATAGCGCAAGGAGGTAGT
 901   ---------+---------+---------+---------+---------+---------+   960
       GGTGACGAAACACACAAATGTTTCACCCCACCTTTTGGATGCCGTAGAGGAGCTCGCTCG
 961   ---------+---------+---------+---------+---------+---------+   1020
       CCAGATTGCTGAAACCGCTAACAAGGCTTATTCCAGCCATTTCAGGCAGATTGTCAAAGT
1021   ---------+---------+---------+---------+---------+---------+   1080
       CCTGCCGCCTGAGGTTCCCGACCTCTACGCCTGGCTGGCCGCCCTGGATGACTCCGCCAT
1081   ---------+---------+---------+---------+---------+---------+   1140
       CGAGGAGCTTGCCCAGCGCCTGAGGGAGGTCGAGGGAAGCCCCCGCCCCCATTTCACCGC
1141   ---------+---------+---------+---------+---------+---------+   1200
       CGCCCTCAAAAAGGCCCTGGCCATCGCCCTACAGCGGCGGACCCTCGCCGAGATGCCCCC
1201   ---------+---------+---------+---------+---------+---------+   1260
       CACGTTCGCCAACGCGCTCCGCTGGGCGATGGAACGGCAAGGGGTGAGCATCCGCAAGCT
1261   ---------+---------+---------+---------+---------+---------+   1320
       TGCGAGAGAGGTAGGGGTCAGCAAAACCACTGTTAAAAAGTGGCGTGGAGGCCGCTTTGT
1321   ---------+---------+---------+---------+---------+---------+   1380
       CCCTCGTTCACGGACCTACGTGAGGAGGTTGGAGGAGATCCTGGACCTCCCGGAAGGCGC
1381   ---------+---------+---------+---------+---------+---------+   1440
       CCTTTCGGGACGACTACCCCGCTGGGGGTTGCCAAAAATATTGGAAGGTGTTGAGGGGAA
1441   ---------+---------+---------+---------+---------+---------+   1500
       AGATGCCCCTTATCCCGGGTTCACGCGGACCTTCCTGCGCGTGGCCGCCCTGGCGCGCTA
1501   ---------+---------+---------+---------+---------+---------+   1560
       CGGCCGCCCGTGGGATGATCTCTCTCCCGACGAACAGGAGGCCCTTCGGCGCGAGGACGA
1561   ---------+---------+---------+---------+---------+---------+   1620
       AGACCGGTGGACCCGCCTCTCCAACCGCCAGAAGCGAGTGCGAAAGGCCAGTCAAAAACC
1621   ---------+---------+---------+---------+---------+---------+   1680
       TTTTCGGCTTTCCTTTGACGAGTGGCCAACTGAGGCTCGCAAAGAATGGGAGGACTACGA
1681   ---------+---------+---------+---------+---------+---------+   1740
       GCGCTATGCCTCATCGGCACCTGGGAGCATCGCGCGCGTGCAGGCGGCGCTTGCGGGCGC
1741   ---------+---------+---------+---------+---------+---------+   1800
       ACCTCTCGCTCCCACGACCGTGCGGACGGAAACGCTCGAGCGTGAGCGGATACTTATAGA
1801   ---------+---------+---------+---------+---------+---------+   1860
```

Fig. 7 (continued)

```
      ACTGTTCTACGGCTACTGTGTAAACGAACGGGGCCTCGACAGCAACGCGTTGAGCCTCGC
1861  ---------+---------+---------+---------+---------+---------+  1920
      CCTCCTCACAGACCTGGAGCTCGTCCAATCGTACCTGGAGTGGCGCGTGAATAGGTACAA
1921  ---------+---------+---------+---------+---------+---------+  1980
      GGACGAGGATTTACCCCCCGTTACTCGATCGGAATACATGTTTATCGCCCTGGTGAAAAA
1981  ---------+---------+---------+---------+---------+---------+  2040
      ACTCCACAGAGGTTATCTCCGCGCCCTTGGGCTTGGGGTAGACCCGGACGGGGTGAAAGA
2041  ---------+---------+---------+---------+---------+---------+  2100
      GCTGGAACGGAAACTGAAAATCGCCGGAATTGATGTCACGGACGGCTACCACGCGGTGGA
2101  ---------+---------+---------+---------+---------+---------+  2160
      GCCCCTCCTGGAAACTCACGAGCCCCTCCGCTGGGTGCTGGATGGCATCCGGCTCATGCT
2161  ---------+---------+---------+---------+---------+---------+  2220
      CCGCGATGCGGCGGGGCGGGTAGGCAACCTGCTGACACCCCAAATCCCCACCGCCAAAAG
2221  ---------+---------+---------+---------+---------+---------+  2280
      CGAAGCGGGCGAAGCGTTCGCCCTCTACCGGGACGTCGTTCTGCTTTGGATGATGGTGGG
2281  ---------+---------+---------+---------+---------+---------+  2340
      CCACCCCCTCCGGGCGAAGCATTACTACGAAGCTCGCTTGGACATGAGCCAGTTCCAAGA
2341  ---------+---------+---------+---------+---------+---------+  2400
      CGGGGATTTCGCTCCCGGGCGGGGACACGTGGGGCGGGCCGGCGGAGGGTACTACCTGGC
2401  ---------+---------+---------+---------+---------+---------+  2460
      CTACCGCAAAGTGGAGTTCAAAAACGCCCGAGGCCAGGTCTTTCAGAGCCTCCAGGACCA
2461  ---------+---------+---------+---------+---------+---------+  2520
      CGATCTCGTCACGTTCCCCCTGGACGACCCCGAGCACCCTGTCCTGGTCCTGGACGTGAA
2521  ---------+---------+---------+---------+---------+---------+  2580
      CGGGATGCGGTACTCCCTCAACGAGCTCTTTCACGTCTACCTGCGCACGATCCTCTCCCG
2581  ---------+---------+---------+---------+---------+---------+  2640
      CCTGGCCCAGGCCTGGGCCGGACCGGTCCCCTCCTGCCCCTGTTTCCGGGTGCCGATACG
2641  ---------+---------+---------+---------+---------+---------+  2700
      AGGCTCAGACTTGCGCACATCGTTCGCAGGCGCGCCGCCTACGTGGCCGCCGTGCCCGGG
2701  ---------+---------+---------+---------+---------+---------+  2760
      GTACCCCAGAAACTTTTGCCCTTCGGCCCCCACTCCATCCGCCACGTGGTGGCCACGGAG
2761  ---------+---------+---------+---------+---------+---------+  2820
      GTCGTGAAGCGCACGGGCTCTTTTGAGGCCGCCGCCAACGTGCTCCTGGATAGCATAGAC
2821  ---------+---------+---------+---------+---------+---------+  2880
      ATGGTCGTTCGACATTACGCCCGTTCGTTCCCCGCGACCGTAACAGTCACGGTTGGCGGG
2881  ---------+---------+---------+---------+---------+---------+  2940
      CTAACGCCCGCGCCCGGGGAGGTGAGCGGTGAGGGACCTCCACGACTTTTTCCTGGCCCG
2941  ---------+---------+---------+---------+---------+---------+  3000
      GGTGGACGAACTGGTGCCGGAACTCCTACCCGGGGCGCGGCGGGTGGGCGACGAGTGGCG
3001  ---------+---------+---------+---------+---------+---------+  3060
      GGCGGGCTCGGTCCAGGGCGAGCGGGGCGACAGCCTGGCCGTGGACCGCGGGAAGGGCTT
3061  ---------+---------+---------+---------+---------+---------+  3120
      CTGGATCGACCACAACCCCTCGGCCCCCGAGCCCCGGCAGGGAAACCTCCTCACGCTGAT
3121  ---------+---------+---------+---------+---------+---------+  3180
      CCAGGCGGCCAAGGGGCTCTCCCCCGAGGAGGCCCGGCGCTGGGCCCAGCAGTGGCTTGG
3181  ---------+---------+---------+---------+---------+---------+  3240
      CCTCTCCCCTTCGCCAAAGGTCAGGCGGACGAGGAGCTCAGGACCAAAGGTCTTGAGTAC
3241  ---------+---------+---------+---------+---------+---------+  3300
      TCAAGTGCGTGGGAGCTCGGGTGCTCCAGTCCCTGAGTCTTCAGGTTCCCAGGTACCTGA
3301  ---------+---------+---------+---------+---------+---------+  3360
      GGAGTCGGACCCCTTTGACAACCCCCGCTTCCGGGACCTCCTCACCCCCAGGGGCGAGGA
3361  ---------+---------+---------+---------+---------+---------+  3420
      CGAGGCCCCCTTGGCCCCGGCCTCCGAGGAGGTGCTGCGGCGCATGGTGTCTAGGCTTCT
3421  ---------+---------+---------+---------+---------+---------+  3480
      CCGCACCCCCGAGGCCGTGGCCTACCTGAAGGGGCGCGGTCTGGATGCCCGGGTGGTCCG
3481  ---------+---------+---------+---------+---------+---------+  3540
      CCGCTTCTACCTCGGCCTGGACGACACCGCGCGGGCCACCGCCGCCCTGGTCTACCCGGT
3541  ---------+---------+---------+---------+---------+---------+  3600
      GATAGGGCCGGACGGCTCCCCCGTTCGCCGCCACCTCTACTACGAGATCCCCGGCCTCAC
3601  ---------+---------+---------+---------+---------+---------+  3660
      CCAGGGCGCCCCGGGCAAGGGCTGGGGAGGGGGAGGCCCACCAGCTACTGGGCCCTCCC
3661  ---------+---------+---------+---------+---------+---------+  3720
```

Fig. 7 (continued)

```
      CCCCTTCGAGGGCCCCTCCCCCCGCCGCAAGCTCTTCTTGTGCGAGGGGGCGAAGGATGC
3721  ---------+---------+---------+---------+---------+---------+  3780
      CTGGGCCCTCTGGCTCCACCTCCACGCCCAGCCCTGGGCCCAGGACCTGGCGGTGGTGAC
3781  ---------+---------+---------+---------+---------+---------+  3840
      CTCCACGCACGGCTCCGCCCTCCCCGAGGCCTGGAAAGACCCCCTGTTCTGGGCCCCTTG
3841  ---------+---------+---------+---------+---------+---------+  3900
      GGAGGAGGTCTACCTGGGCCAGGACGCCGACTCCGCCGGCGAGGAGATGGCCCGGAAGGT
3901  ---------+---------+---------+---------+---------+---------+  3960
      GGCGGAGGTGGCGAGGCGGCCCGTCCGCCGCGTCCGGGTCCCGGAGGGGATGGGAAGGA
3961  ---------+---------+---------+---------+---------+---------+  4020
      CTGGACGGACTACTTCCTGGCGGGGGGCACCCCCGAGGGCTTGCGCCTCCTCCTGGAGGG
4021  ---------+---------+---------+---------+---------+---------+  4080
      AGCGGAGGTCTGGGAAGAAGAAGTGGCTGGAGGTGGGGCCAGGATCCAGCTCCCGGACCC
4081  ---------+---------+---------+---------+---------+---------+  4140
      CGTGGACATCCAGCGGGCCTTCGTGCGGGGCCACCTCTACGTCCCCGTGCGGGTCCTGGA
4141  ---------+---------+---------+---------+---------+---------+  4200
      GAACCGGGGGGAAGAAGGGGCCCGCTACCGCACCGTGGTGGTCCGCTCCGACGGGGCCGT
4201  ---------+---------+---------+---------+---------+---------+  4260
      CCTGGGCTGGGGCTACTTGCCGGCCCCGCCCGGCACCCCCTTGGAGGACCGGGTGCTGGC
4261  ---------+---------+---------+---------+---------+---------+  4320
      CGTGGACGACGGCACCATCATCCGCAGGCCCCCGAAGGCGGCCGCCGGGACCTCGTGGAA
4321  ---------+---------+---------+---------+---------+---------+  4380
      CGGGGAGGCCATCAACCGCTTCCTGGAAGCCCGGGCCCGGGGAGTGAGCGCCATGACCGT
4381  ---------+---------+---------+---------+---------+---------+  4440
      GGCCCCCCGGGACCTGCCTGGGCTCATCGTCCGCCACCTCCGCCAGGTGATCCTCCCCAG
4441  ---------+---------+---------+---------+---------+---------+  4500
      TGAGGACGGCTACCTCCTGGCCGCCTTAGGGGTCATGACCTCCTACGTGCAGAGCGTCTT
4501  ---------+---------+---------+---------+---------+---------+  4560
      CGACGCCGTGCCCCTCTTCCTCGTGGTGGGCCCGCCGGGCTCGGGGAAGACGGAGTTCGC
4561  ---------+---------+---------+---------+---------+---------+  4620
      CCGCCTCATGGCCGAGCTGGGGGCCAACGGCGTGGTGATCACCGGCCAGACCTCCGCCGC
4621  ---------+---------+---------+---------+---------+---------+  4680
      CACCGCCGCCCGGATCATCGACGAGACGGGGGGGCTGGTGGCCTTCGACGACCTGGAGGA
4681  ---------+---------+---------+---------+---------+---------+  4740
      GGTGCGCCAGCGGTCGGGGAGCGCTGAGGCCTCCCAGCTGGAGCAGTTCCTCAAGGTGTC
4741  ---------+---------+---------+---------+---------+---------+  4800
      CTACAAGAAGGAGACCGCGGTCAAGAGCTGGACGGACACCAAGGGGATGCGGGTCCTCAC
4801  ---------+---------+---------+---------+---------+---------+  4860
      CCTCAACTTCTTCGGGGTCAAGGTGATCACCAACACCCAGGGGACGGGGGACATCCTGGG
4861  ---------+---------+---------+---------+---------+---------+  4920
      GAGCCGGATGCTGGTCATCCGCACCGCCCGCCTCCGGGACCTGGGCAGAGGGGAGGAGCG
4921  ---------+---------+---------+---------+---------+---------+  4980
      CCGCCCCGAGGGGCTCTCCCCCCCAGGCCCTCCAAGAACTCCGGGACAACCTCTACATCT
4981  ---------+---------+---------+---------+---------+---------+  5040
      GGGCCATGGAGAACGCGGCCAGCCTCCACGCCCTGTACCGGGAGCGCTTCGCGGGCAAGG
5041  ---------+---------+---------+---------+---------+---------+  5100
      GGGAGCGCCTGGACGAGATCGCCGCCCCCTTGCGTACCATCGCCCACCACCTGGGGGACG
5101  ---------+---------+---------+---------+---------+---------+  5160
      AGGAGCTGGCGGCCCGCCTGGAGGACGCCCTGCGCCGGCAGGAAGGGCGCCTGGAGGAGA
5161  ---------+---------+---------+---------+---------+---------+  5220
      CCCTTTCCGATGCCGAGGTGGTGGAGACCGCCCTCAAGGAGGCCATCCGCCAGGGCTACC
5221  ---------+---------+---------+---------+---------+---------+  5280
      GGAGCCACGTGGCCCTGGTCCACGTGATCTTCCAGGCCCGGAAGATCTTCGGGGACGACT
5281  ---------+---------+---------+---------+---------+---------+  5340
      GGGGCCGGGAGCGCACCGTGGACATCCCCCGGTGGCGGGACCCCAAGTGGGTGGGGCAGA
5341  ---------+---------+---------+---------+---------+---------+  5400
      TCGCCAGCAACTACGGCTGGGCGGCCCCAGAAAGGCCCGTGAGGCCCCGGCTTTGGGACA
5401  ---------+---------+---------+---------+---------+---------+  5460
      AGCAGTTCCGCATCATGCGCCTGGAGCCCACCTTCGTGGAGCGGGTGGTCAGGGGCTTCC
5461  ---------+---------+---------+---------+---------+---------+  5520
      TCCAGGAGGGGATCCCCTTGGAGCCCCTGAAGCAACCCCTGGCTTCTGCCTGGACACCCC
5521  ---------+---------+---------+---------+---------+---------+  5580
```

Fig. 7 (continued)

```
     CTGCGCCGAGTGCGCCTACCTGCACTGGTGCGACCTCCGGCCTGACAAGGAAAAGTGGCT
5581 ---------+---------+---------+---------+---------+---------+ 5640
     GGAGCGCTACGGGGAGGCCAAGCTGGCCCAGAAAAGGCGGGAGCTGGAGGAGGAGTTTTT
5641 ---------+---------+---------+---------+---------+---------+ 5700
     GGCCCTGGTGGGGCCCCAAGATGGCCTTGGCCTCCAGGCTTCCGCCGAGGAGGAGGGAGA
5701 ---------+---------+---------+---------+---------+---------+ 5760
     CCGAGGTAAGCACCCAAGTACCCAAGTACCCAAGACCCTAAAGCCTCAGGTACCGGAGGA
5761 ---------+---------+---------+---------+---------+---------+ 5820
     CCTCGGGGACGGAGGACCTAAAACCCCAAGGGCGTGAAAGACTGAGGTGAGAGGGATGAT
5821 ---------+---------+---------+---------+---------+---------+ 5880
     CGTGGCTGTCACCGGCTTCAAGGGAGGGGTGGGGAAGACCACCACGGCGGTCCACCTGGC
5881 ---------+---------+---------+---------+---------+---------+ 5940
     CTGCTTCCTGGCCGAGCGGGGCCCCACCCTGCTGGTGGACGGGGACCCCAACCGCTCCGC
5941 ---------+---------+---------+---------+---------+---------+ 6000
     CACGGGGTGGCACCGGAGGGGAGGCCTCCCGGTGACCGTGGTGGACGAGCGGGTGGCGGC
6001 ---------+---------+---------+---------+---------+---------+ 6060
     CCGGTACGCCCGGGAGCACGCCCACGTGGTCATAGACACCCAGGCCCGCCCCACGGAAGA
6061 ---------+---------+---------+---------+---------+---------+ 6120
     GGACCTCCGGGCCCTCGCCAAGGGGGTGGACCTGCTGGTCCTGCCCACGTCCCCCGACGC
6121 ---------+---------+---------+---------+---------+---------+ 6180
     CCTGGCCCTGGAGGCCCTCCTGGCCACCCTGGAAGCCCTGCGGGGGGCGGAGGCCCGCTT
6181 ---------+---------+---------+---------+---------+---------+ 6240
     CCGGGTCCTCCTGACCATGGTGCCCCCGCCCCCGAGCCGGGACGGGGAGGAGGCCCGGGC
6241 ---------+---------+---------+---------+---------+---------+ 6300
     CCTCTTGGGGGCGGAGGGCGTTCCCCTCTTCACAGGCTGGGTGAGGCGGGCGGCAGCCTT
6301 ---------+---------+---------+---------+---------+---------+ 6360
     CCCCAAGGCCGCCCTCCTGGGGGTGCCTGTCTACCGGGTGCCCGACCCCAGGGCGAGGCT
6361 ---------+---------+---------+---------+---------+---------+ 6420
     GGCCTGGGGGGACTACGCGCGGGTGGGGGAAGAGCTCCTGAAGGAGGTGGGGGGATGAGC
6421 ---------+---------+---------+---------+---------+---------+ 6480
     AAGTTCGCCAGGCTCCTCAAAGAGGTCAAGGAGAAGGAGGAGGCCTCCGGGGAGCGGCCT
6481 ---------+---------+---------+---------+---------+---------+ 6540
     CGGGGGAAGAGCCGGCGGGAGGACTACGTGGCCATGAAGGTCTACATCAGCAAAGAGCTT
6541 ---------+---------+---------+---------+---------+---------+ 6600
     CACCGGAGGCTGAAGCTGAAGGCCCTGGAGGAGGAGAAGGAGCTTTCGGAGCTGGTGGAA
6601 ---------+---------+---------+---------+---------+---------+ 6660
     GAGGCCCTGAGGAAGTTGCTGGTGTGACCTCCTCCCGCCTCGTAGAGCGTGAAAAGGAGG
6661 ---------+---------+---------+---------+---------+---------+ 6720
     TAAGACGATGGTCACCCTTAACAAATCGCCCCTAGAAGCCCTCTACGCGGGCCACTCCCC
6721 ---------+---------+---------+---------+---------+---------+ 6780
     CCAGGAGGCGGGCCGTCTCTTCGAAGCGCCTGGTCCGCAAGATATTGAAGGAACTCCACC
6781 ---------+---------+---------+---------+---------+---------+ 6840
     CCATCTGGAGCCAAGAGTTCGTGGATGTCGTCCCTTGGTCCGAGCACGCCACCCGCAAGG
6841 ---------+---------+---------+---------+---------+---------+ 6900
     GGCTCAGGGCCACGGACATCGGCGTGGACCTGGTGGGCTACGGGAAGGACGACAAGGTCT
6901 ---------+---------+---------+---------+---------+---------+ 6960
     ACGCCATCCAGGTCAAGCTGTGGGATAAGCCCCTCTCTTGGAAGGACCTGGGGAGCTTCG
6961 ---------+---------+---------+---------+---------+---------+ 7020
     TGGGGGTGGTGAACCACCCCGAGTACGGCTTCGACCACGGGCTCATCGTGGCCCCAAGAG
7021 ---------+---------+---------+---------+---------+---------+ 7080
     GCGTGACCCAGGAGGCCGACCGCCAGCTCCAGGGCCTACCCATCACCATCCTGAGCGAAG
7081 ---------+---------+---------+---------+---------+---------+ 7140
     AGGCTCTCCTAGAAGACCTGGACCTGGAATCCCTCGTTCCAGACCGCCCCGAGGAAGCCC
7141 ---------+---------+---------+---------+---------+---------+ 7200
     GCAGGCGGGGGAAGAAGGCCCTCCGTAAGTACCAGCAAGAAGCCTTAGAGGAGGTGGCCA
7201 ---------+---------+---------+---------+---------+---------+ 7260
     AAGCCTTCTTAGAGAAGGGCCTGCCCCGGGGCAAGCTCATCATGCCCCCGGGCACGGGCA
7261 ---------+---------+---------+---------+---------+---------+ 7320
     AGACCCTGGTGGCCCTCAAGATCGCCGAAAAGGTGGCGGCCCCGGGGGAGGGTCCTCT
7321 ---------+---------+---------+---------+---------+---------+ 7380
     TCCTGGCGCCCTCCATCGCCCTCCTGGACCAGTCCCTCAGGGCCTGGGCGGCGGAGGCTT
7381 ---------+---------+---------+---------+---------+---------+ 7440
```

Fig. 7 (continued)

```
          CCTTGCCCTTGCGCCTCTTCGCCGTGGTCTCGGACACGGGCGTGGGCAAGACCTCGGAGG
    7441  ---------+---------+---------+---------+---------+---------+  7500
          ACGACCTCTCCGCCCTCTCCCTCCTCTCCATCCCTCCTACCACCAAGCCTGAGGAGCTGG
    7501  ---------+---------+---------+---------+---------+---------+  7560
          CCTCCGAGGCCAAGACGGAGAGTCAGGAGGCCCTCACCGTGGTCTTCTCCACCTACCAGT
    7561  ---------+---------+---------+---------+---------+---------+  7620
          CGGCGGAGGTCCTGGAGAGGGCCCAGAAGGAGCACGGGCTTCCCCCTTTTGACCTGATGA
    7621  ---------+---------+---------+---------+---------+---------+  7680
          TCCTGGACGAAGCCCACCGCACAGCCACGGTGCGGGCGGGAGAAGAAAGCCCCTTCACCA
    7681  ---------+---------+---------+---------+---------+---------+  7740
          AGGTGCACCACGACCACTACGTGAAGGCCCGCCACCGCCTCTACATGACGGCCACGCCCA
    7741  ---------+---------+---------+---------+---------+---------+  7800
          GGATCTGGGAGGTGGAGGGGAATGGAGAGAGGGGCCAAGGGAAAAAGGCGGGGAAAAAGA
    7801  ---------+---------+---------+---------+---------+---------+  7860
          AGGACCCTCAGAAAGAGGGTTCTCCTCCCCTTTTGGACCTCGGTGCCTCTCCTACGGAGG
    7861  ---------+---------+---------+---------+---------+---------+  7920
          ACTCCACGGCCCCCGAAGGGGTGGAACTCCTGGTCTACTCCATGGACAACGAGGGGATCT
    7921  ---------+---------+---------+---------+---------+---------+  7980
          ATGGCCCCACCCTCTACGAGTACACCTTCACCCGCGCCGTGAAGGAGGGCCACCTGAGCG
    7981  ---------+---------+---------+---------+---------+---------+  8040
          ACTACAAGGTCATCGTCTTCTCCGTGGCGGAGGAAGCCCAAAAGGACCTGGCCTCCTACC
    8041  ---------+---------+---------+---------+---------+---------+  8100
          TCCAGGGACCCGAGGCCCTCAAGGTGGAGGAGGCTCTGAAGGCCCTGGGCCTGTGGAAGG
    8101  ---------+---------+---------+---------+---------+---------+  8160
          TCCTCCAGGGGGAGGTGCGGGACGAGGAGGGGAACCCGATGGGGGGCCTCGACCTGCGGA
    8161  ---------+---------+---------+---------+---------+---------+  8220
          GAGTCATCGCCTTCCACGGCCGGGTGAAGGAGTCCAAGGAGATGGAGGAAGAGTTCACGA
    8221  ---------+---------+---------+---------+---------+---------+  8280
          AGGTGGCCCTCGCTGCCCAGCAGGCTGGCCTCCTTCCCGAGGAGCTCCGGCGGGTGGAGG
    8281  ---------+---------+---------+---------+---------+---------+  8340
          TGAAGCACATAGACGGGCAGATGTCCGCCTATGACCGGAAGCGCCTCCTGGACTGGCTTA
    8341  ---------+---------+---------+---------+---------+---------+  8400
          GGGAGAACGTCCCCGAGGGGGAGGTCCGCCTCCTCACCAACGCCAAGGTCCTCACCGAGG
    8401  ---------+---------+---------+---------+---------+---------+  8460
          GGATCGACGTCCCGGCCCTAGATGCCGTGGCCTTCATGCGTCCCCGGGACAGCGTGGTGG
    8461  ---------+---------+---------+---------+---------+---------+  8520
          ACGTGATCCAGGCCGTGGGGCGGGCCATGCGCAAGGCCCCGGGCAAGGAGTACGGGTACG
    8521  ---------+---------+---------+---------+---------+---------+  8580
          TGGTCCTGCCCGTGGTGGTGAGGGGGCAGGACGAGGAGCGGGAGATCGAGGAGAGCGGCT
    8581  ---------+---------+---------+---------+---------+---------+  8640
          ACCGGGCGGTGTGGCAGGTGCTCTCGGCCTTGCGCTCGGTGGACAAGTCCTTCGAGGCCC
    8641  ---------+---------+---------+---------+---------+---------+  8700
          GCATGCGGCCCCCCCTGGTGCGCCTCTCGGGTAAGGGCGAGGGCGGGGAAGGTGGAGAGG
    8701  ---------+---------+---------+---------+---------+---------+  8760
          CCCGAGAGGGTGTGGCCGTCATCGGGGAAGGAAGCGCCTCCCCCGTGATCGTAGATGTCC
    8761  ---------+---------+---------+---------+---------+---------+  8820
          TTCAGGGGAACCTCAACCTCCACCAGGAGATCACCCGGAGCCTCGCCGGCAAGCTGGTCA
    8821  ---------+---------+---------+---------+---------+---------+  8880
          GGCGCCTCGCCCTGGGGCGGAAGTACCTGGAGAACTGGGCCCAGGACGTGGCCCGGGTGG
    8881  ---------+---------+---------+---------+---------+---------+  8940
          CGAAGGTGCTGGAGCAGCAGGTCAGGGCGATGGCGGAGCGGGACCCCAAGGTGAAGGAAA
    8941  ---------+---------+---------+---------+---------+---------+  9000
          AACTGGGGAAACTCCTCGCCGCCCTGCAGGCCTTCACCAGCGAGAGCGTGACGGAGGACG
    9001  ---------+---------+---------+---------+---------+---------+  9060
          AAGCCATCCTCATGCTGGTCCAGCACGCTCTCACCAAGCCCATCTTCGACGCCCTCTTCG
    9061  ---------+---------+---------+---------+---------+---------+  9120
          GGGAACTCCTAGAAAAGCGGGAGGACCCCGTTTCCCGGGCCCTAGACGAACTCTTCCAGG
    9121  ---------+---------+---------+---------+---------+---------+  9180
          AGTTCAGGGGGTTCCTGGACCGGGAAGGGGAGGCCCTCAAGGATTTCTACGAAGAGATGC
    9181  ---------+---------+---------+---------+---------+---------+  9240
          GCCTCAAGGCCCTAGGGCTCACGGACGAAGCCGAAAGGGCCGACTTCCTACGGAGGCTCT
    9241  ---------+---------+---------+---------+---------+---------+  9300
```

Fig. 7 (continued)

```
         ACTCCAACTTCTTCGCCCGGGCCTTCCCCCAGGTGGCCGACCAGGTGGGGATCGCCTACA
   9301  ---------+---------+---------+---------+---------+---------+  9360
         CCCCGGTGGAGCTGGTGGACTTCCTGGTGAAGAGCGCAGACGAGCTGGCCAGGAAGCACT
   9361  ---------+---------+---------+---------+---------+---------+  9420
         gTTGGCCGGGGGCTCGATGGGGAGAAGGTCTTCATCCTGGAGCCCTTCGCCGGCACAGGC
   9421  ---------+---------+---------+---------+---------+---------+  9480
         ACCTTCGTCACCCGAATCCTGCACCGGGTAGCCGAAAgGGGCGGGGCCGACGCGGTCAAG
   9481  ---------+---------+---------+---------+---------+---------+  9540
         GGCAAGCTGGAGCGGGGGGAGATCTGGGCCAACGAGATCCTTCTCCTCCCCTACTACGTC
   9541  ---------+---------+---------+---------+---------+---------+  9600
         CTCAGGGCCAACGTGGAGAACACCACCCTGGCCCTGACCGGGGAGTACGTCCCCTTCAAG
   9601  ---------+---------+---------+---------+---------+---------+  9660
         GGGGCGTTCTGGCGGACTCCTTCGGCTGGCGGAGCTGGGGTATAGCGAGAAAAAGTTTGG
   9661  ---------+---------+---------+---------+---------+---------+  9720
         CATCATCCCGCTCTTCCCGGAAGAATACGGTGAGGCCCTGAACGAGCAGCTGAAGGCCCC
   9721  ---------+---------+---------+---------+---------+---------+  9780
         TATCCAGGTTATCCTCTCCAACCCCCCGTGCGGGCTTGGTTGGAGAAGGAGGGCGAGGGG
   9781  ---------+---------+---------+---------+---------+---------+  9840
         AAGAAGAACCCCGTCTACCGTAAGGTGCGGGAGCGGGTGGAGCCAACCTATGTACGGCGG
   9841  ---------+---------+---------+---------+---------+---------+  9900
         GCCAAGGAACTTCCCATCGGGGGGACAAAACCCAAGGGAGAGAACCTGAACTCCCTCTAC
   9901  ---------+---------+---------+---------+---------+---------+  9960
         GACCAGTACATCCAGGCCTTGCGGGTGGCGAGCGACCGTATCGGGGAGGAGGGGGTCGTG
   9961  ---------+---------+---------+---------+---------+---------+  10020
         GCCTTCGTCACCAACAACGGGTGGCTGGGGGGCGTAGTGCCCCGGGGCTTGCGGGCCTCT
  10021  ---------+---------+---------+---------+---------+---------+  10080
         TTGGCGGAGGAGTTCGCCGAGGTGTACGTCTACGACCTGAGGGGGGATGCGAGGGAGAAG
  10081  ---------+---------+---------+---------+---------+---------+  10140
         GGGGAGGCACGGAAGAAGGAGGGGGGCGGGGTCTTTGGACAGCCTTCCCGCGCCGGGGTC
  10141  ---------+---------+---------+---------+---------+---------+  10200
         TGCCTCCTCCTCCTGGTGAAGCGTAAGGACCACAAAGGGATCGGCAAGGTCCACCTCTAT
  10201  ---------+---------+---------+---------+---------+---------+  10260
         CGGGTCGGGGACGGCCTCTCCCGGGAGGCCAAGCTGGCTCTGGTGAAGGAGCATGGCTCA
  10261  ---------+---------+---------+---------+---------+---------+  10320
         GTCTCTGGGTTCCCTGGCAAGAGGTTCCCTATGAAGAGTGGGTGGGGAGGCTTACCCCCG
  10321  ---------+---------+---------+---------+---------+---------+  10380
         GGTTCTCGGGGATGTTGTCCCTGGACGAGGTCTTTGAGGTGCGGAGTTCTGGGGTGAAGA
  10381  ---------+---------+---------+---------+---------+---------+  10440
         CCAACCGCGATGCCTACGTCTTCAACCCCTCCCGGGCGGAGCTGGAGCGGCACATGAGGC
  10441  ---------+---------+---------+---------+---------+---------+  10500
         GGCTCATCTCCACCTACAACGAGCACGTGAAAAGGAAAAAAGAGGGGAAACTAGGGGAAC
  10501  ---------+---------+---------+---------+---------+---------+  10560
         TGGAAAAGGATGAGAGCATCATCAAGTGGGATAGGGAACTCATCAGGTACCTAGAGTCCC
  10561  ---------+---------+---------+---------+---------+---------+  10620
         TGAGGGAAGCTTCCTACGAAGGGAGCGGTCAAGTCTACGAGGCCCTCTACCGCCCCTTCG
  10621  ---------+---------+---------+---------+---------+---------+  10680
         TGCCTATGTACCTCTACCTCAGCCGCACTTTCAATAGCATGATTTACCAAATCCCCCGCA
  10681  ---------+---------+---------+---------+---------+---------+  10740
         TCTGGCCCACCCCCGAGGCCGAGAACCTGGCCATCGCCGTGGCCGGAAAGGGGAGTAACG
  10741  ---------+---------+---------+---------+---------+---------+  10800
         CTTTTAGCGCTGTGGCCACCAGGAGGGTGGTTGACCTGCACTTTATTGAGACCACCCAGC
  10801  ---------+---------+---------+---------+---------+---------+  10860
         TCTACCCCCTTTACCACTACCCCGAAAACAGCCCTCTGGGGGACACCCAAAGCGCAAGC
  10861  ---------+---------+---------+---------+---------+---------+  10920
         TCAACCTCAAGGAGGAGTTCTTGAGGAAGCTTGGGGAGGTCCTCGGCCGCCCCGTTCCCC
  10921  ---------+---------+---------+---------+---------+---------+  10980
         CCGAGGAGGCCTTCGCTTACATCTACGCCGTGGTGAGCCACCCCCTCTACGCCGAGCGCT
  10981  ---------+---------+---------+---------+---------+---------+  11040
         TCGCCAAGGACCTCAAGATGGACCTCCCCCGCATTCCCCTCCCCCAAGATCCCGAACTCT
  11041  ---------+---------+---------+---------+---------+---------+  11100
         TTGCCAGGCTGGTGAAGGCGGGTCAAGAACTCATTCACCTCCACACCGAGTACGAGACCC
  11101  ---------+---------+---------+---------+---------+---------+  11160
```

Fig. 7 (continued)

```
         TGCCCCCCTGGAGCCCAGTCCCCCTTCGGGTGGAAGAGGGAGGCCCGGAGGACCCTACGA
11161    ---------+---------+---------+---------+---------+---------+    11220
         GCGCTACCGGGTGGAGCGGATGAGGCTGGACAAGGAGAGGAGGGTTCTCCAGTACAACGA
11221    ---------+---------+---------+---------+---------+---------+    11280
         CTGGGTCCGGGTGGAGGGCATCCCCGAGGAGGCCTTCCGCTGGCGCCCCGGGGGGTACTC
11281    ---------+---------+---------+---------+---------+---------+    11340
         CCCCTTGGAGTGGATTGGCCGCTTCTGGAAGGTGGAGGAGAAGGTGCCCAAGGGCAGGGG
11341    ---------+---------+---------+---------+---------+---------+    11400
         GGAGGCCATCGTCTGGGACCCCAACCTCTTCCTCAAGGAGAAGGGGGAACCCCGTTACCT
11401    ---------+---------+---------+---------+---------+---------+    11460
         CCTGGACCTCATCGGGCGGGCGGTCCAGGTGGCCGTGCAGACGGTTGGGATCCACGAGGA
11461    ---------+---------+---------+---------+---------+---------+    11520
         GCTGAGAGAAGACGTGGAAGCTCTGCTGGGTTGAGGGGGTGCTGGCCCGCCGTTCTCCCT
11521    ---------+---------+---------+---------+---------+---------+    11580
         ACTCCTTTAGGGCCTACCCCTACGATCCAAGCACGGCCCTGGGGGGCGCTCAGGTGGGCA
11581    ---------+---------+---------+---------+---------+---------+    11640
         TCCCACGTCCAAGGCCCCGACTTGGGCACCCCATGCTGCGAACTTACAGCCCAAGGGCCT
11641    ---------+---------+---------+---------+---------+---------+    11700
         GAAACATTCCCCCCTGCTCACGGGGGAAAGTTCGTGAAGGAAAGAGCAAAGCCTTTTTTA
11701    ---------+---------+---------+---------+---------+---------+    11760
         TCGCATCCGGAGAGATGGCGGGGTGGAACTTTTCCCCGAGGACTCCCCCATAGGGACATG
11761    ---------+---------+---------+---------+---------+---------+    11820
         TAAACGGCAAGCTATCAGTGTAGACTTTTTTCAAAAAGAGCCATACTCGTGTTTTCCCGT
11821    ---------+---------+---------+---------+---------+---------+    11880
         TCAGAACGGCATTTTTGCTAAGGAGGTGGTTTACAAATGGGTGTTAATGCGCTACATCCT
11881    ---------+---------+---------+---------+---------+---------+    11940
         CCGGTAGTAGGAGCATGC
11941    ---------+--------    11958
```